

Replace the paragraph beginning at page 6, line 4, with the following rewritten paragraph:

Fig. 2A-2B are a set of diagrams that depict the characteristics of long discordant helix segments. Amino acid sequences, together with determined and predicted secondary structure elements for sequences having  $\geq 9$ -residue discordant segments are shown. Also shown are those discordant segments of A $\beta$ , mouse PrP, and human PrP. The proteins are grouped by the length of their discordant stretch. The experimentally determined helical segments are drawn as blue cylinders in the bottom row of each case in which the amino acid sequences and residue positions in the PDB entries of the corresponding proteins are given (Top to bottom in each set: Set 16 contains SEQ ID NOs:4-6; Set 15 contains SEQ ID NOs:7 and 8; Set 8 contains SEQ ID NO:9; Set 13 contains SEQ ID NOs:10 and 11; Set 12 contains SEQ ID NOs:12 and 13; Set 10 contains SEQ ID NOs:14 and 15; Set 11 contains SEQ ID NOs:16-18; Set 9 contains SEQ ID NOs:19-20 (top row left to right) and 21-23 (bottom row left to right). The locations of the  $\beta$ -strands predicted by PHD are visualized by yellow strands in the middle row of each case, wherein the reliability index for each residue is shown. The Chou-Fasman-based predictions averaged for 6-residue segments are plotted above residue 3 in each segment and given in the top row of each case. E and e denote extended structures (i.e.,  $\beta$ -strands) predicted with high and low probability, respectively, as in Chou and Fasman (1978, Adv. Enzymol. 47:45-148), and H and h represent predicted helical structures in an analogous manner.--

Replace the paragraph beginning at page 6, line 18, with the following rewritten paragraph:

Fig. 3 is a diagram that depicts the amino acid sequence (bottom row; SEQ ID NO:24) and predicted secondary structure by PHD and according to Chou-Fasman analysis for a polyleucine analogue of SP-C (lung surfactant protein C). The PHD predictions including reliability indices are given in the middle row and the Chou-Fasman data in the top row, but in this case an  $\alpha$ -helix is predicted by both methods, symbolized by a blue cylinder for the PHD prediction.--